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TECH CENTER 1800/2900

## **RAW SEQUENCE LISTING**

PATENT APPLICATION: US/08/913,644

DATE: 10/07/2003

TIME: 13:59:02

Input Set : A:\19424PC Seq List.txt  
Output Set: N:\CRF4\10072003\H913644.raw

4 <110> APPLICANT: Hofmann, Kathryn J.  
5 Jansen, Kathrin U.  
6 Neeper, Michael P.  
8 <120> TITLE OF INVENTION: DNA ENCODING HUMAN PAPILLOMAVIRUS TYPE  
9 18  
11 <130> FILE REFERENCE: 19424PC  
13 <140> CURRENT APPLICATION NUMBER: 08/913,644  
> 14 <141> CURRENT FILING DATE: 1997-11-21  
16 <150> PRIOR APPLICATION NUMBER: PCT/US96/03649  
17 <151> PRIOR FILING DATE: 1996-03-18  
19 <150> PRIOR APPLICATION NUMBER: 08/408,669  
20 <151> PRIOR FILING DATE: 1995-03-22  
22 <150> PRIOR APPLICATION NUMBER: 08/409,122  
23 <151> PRIOR FILING DATE: 1995-03-22  
25 <160> NUMBER OF SEQ ID NOS: 16  
27 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
29 <210> SEQ ID NO: 1  
30 <211> LENGTH: 1524  
31 <212> TYPE: DNA  
32 <213> ORGANISM: Artificial Sequence  
34 <220> FEATURE:  
35 <223> OTHER INFORMATION: HPV18 L1 Consensus Sequence  
37 <400> SEQUENCE: 1  
38 atggcttigt ggccgcctag tgacaatacc gtataccttc caccccttc tgtggcaaga  
39 gttgtaaata ctgtatgatta tgtgactcgc acaagcatat tttatcatgc tggcagctc  
40 agattattaa ctgttgtaa tccatatttt aggttcctg cagggtgggg caataagca  
41 gatattccta aggtttctgc ataccaatat agagtatttc gggtcagtt acctgacc  
42 aataaatttg gtttacctga taatagtatt tataatcctg aaacacaacg tttatgtgt  
43 gcctgtgctg gagtggaaat tggccgtggc cagcctttag gtgttggcct tagtggcata  
44 ccattttata ataaaattaga tgacactgaa agtccccatg ccgcctacgtc taatgttt  
45 gaggacgtta gggacaatgt gtctgttagat tataaggaga cacagttatg tattttgggg  
46 tgtgcccctg ctatggggaa acactgggct aaaggcactg ctgtaaatc gcgtccctta  
47 tcacagggcg attccccccc tttagaactt aagaacacag ttttggaaaga tggtgatato  
48 gtagatactg gatatggtgc catggacttt agtacattgc aagataactaa atgtgaggta  
49 ccattggata tttgtcagtc tatttgtaaa tatcctgatt atttacaaat gtcgtcagat  
50 ccttatgggg attccatgtt ttttgctta cgacgtgagc agcttttgc taggcatttt  
51 tggaaataggg caggtaactat gggtgacact gtgcctcaat ccttatatat taaaggcac  
52 ggtatgcgtg cttcacctgg cagctgtgtg tattctccct ctccaagtgg ctctattgtt  
53 acctctgact cccagttgtt taataaacca tattggttac ataaggcaca gggtcataa  
54 aatggtatct gctggcataa tcaattattt gttactgtgg tagataaccac tcgttagtac  
55 aatttaacaa tatgtgcttc tacacagctc cctgtacctg ggcaatatga tgcattacaa  
56 tttaagcagt atagcagaca tggtaagaa tatgatttgc agtttatttt tcagttatgt  
57 actattactt taactqcaga tggatgtcc tatattcata qtatqaataq cagttatgtt

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58 gaggattgga actttgggtgt tcccccccg ccaactacta gtttgggta tacatatcgt 1260  
 59 tttgtacaat ctgttgctat tacctgtcaa aaggatgctg caccagctga aaataaggat 1320  
 60 ccctatgata agttaaaagt ttggaatgtg gatttaaagg aaaagtttc tttggactta 1380  
 61 gatcaatatac cccttggacg taaaattttg gttcaggctg gattgcgtcg caagcccacc 1440  
 62 ataggccctc gtaaacgttc tgctccatct gccactacgt cttctaaacc tgccaagcgt 1500  
 63 gtgcgtgtac gtgccagggaa gtaa 1524  
 65 <210> SEQ ID NO: 2  
 66 <211> LENGTH: 507  
 67 <212> TYPE: PRT  
 68 <213> ORGANISM: Artificial Sequence  
 70 <220> FEATURE:  
 71 <223> OTHER INFORMATION: HPV18 L1 Consensus Sequence  
 73 <400> SEQUENCE: 2  
 74 Met Ala Leu Trp Arg Pro Ser Asp Asn Thr Val Tyr Leu Pro Pro Pro  
 75 1 5 10 15  
 76 Ser Val Ala Arg Val Val Asn Thr Asp Asp Tyr Val Thr Arg Thr Ser  
 77 20 25 30  
 78 Ile Phe Tyr His Ala Gly Ser Ser Arg Leu Leu Thr Val Gly Asn Pro  
 79 35 40 45  
 80 Tyr Phe Arg Val Pro Ala Gly Gly Asn Lys Gln Asp Ile Pro Lys  
 81 50 55 60  
 82 Val Ser Ala Tyr Gln Tyr Arg Val Phe Arg Val Gln Leu Pro Asp Pro  
 83 65 70 75 80  
 84 Asn Lys Phe Gly Leu Pro Asp Asn Ser Ile Tyr Asn Pro Glu Thr Gln  
 85 85 90 95  
 86 Arg Leu Val Trp Ala Cys Ala Gly Val Glu Ile Gly Arg Gly Gln Pro  
 87 100 105 110  
 88 Leu Gly Val Gly Leu Ser Gly His Pro Phe Tyr Asn Lys Leu Asp Asp  
 89 115 120 125  
 90 Thr Glu Ser Ser His Ala Ala Thr Ser Asn Val Ser Glu Asp Val Arg  
 91 130 135 140  
 92 Asp Asn Val Ser Val Asp Tyr Lys Gln Thr Gln Leu Cys Ile Leu Gly  
 93 145 150 155 160  
 94 Cys Ala Pro Ala Ile Gly Glu His Trp Ala Lys Gly Thr Ala Cys Lys  
 95 165 170 175  
 96 Ser Arg Pro Leu Ser Gln Gly Asp Cys Pro Pro Leu Glu Leu Lys Asn  
 97 180 185 190  
 98 Thr Val Leu Glu Asp Gly Asp Met Val Asp Thr Gly Tyr Gly Ala Met  
 99 195 200 205  
 100 Asp Phe Ser Thr Leu Gln Asp Thr Lys Cys Glu Val Pro Leu Asp Ile  
 101 210 215 220  
 102 Cys Gln Ser Ile Cys Lys Tyr Pro Asp Tyr Leu Gln Met Ser Ala Asp  
 103 225 230 235 240  
 104 Pro Tyr Gly Asp Ser Met Phe Phe Cys Leu Arg Arg Glu Gln Leu Phe  
 105 245 250 255  
 106 Ala Arg His Phe Trp Asn Arg Ala Gly Thr Met Gly Asp Thr Val Pro  
 107 260 265 270  
 108 Gln Ser Leu Tyr Ile Lys Gly Thr Gly Met Arg Ala Ser Pro Gly Ser  
 109 275 280 285

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110 Cys Val Tyr Ser Pro Ser Pro Ser Gly Ser Ile Val Thr Ser Asp Ser  
111 290 295 300  
112 Gln Leu Phe Asn Lys Pro Tyr Trp Leu His Lys Ala Gln Gly His Asn  
113 305 310 315 320  
114 Asn Gly Ile Cys Trp His Asn Gln Leu Phe Val Thr Val Val Asp Thr  
115 325 330 335  
116 Thr Arg Ser Thr Asn Leu Thr Ile Cys Ala Ser Thr Gln Ser Pro Val  
117 340 345 350  
118 Pro Gly Gln Tyr Asp Ala Thr Lys Phe Lys Gln Tyr Ser Arg His Val  
119 355 360 365  
120 Glu Glu Tyr Asp Leu Gln Phe Ile Phe Gln Leu Cys Thr Ile Thr Leu  
121 370 375 380  
122 Thr Ala Asp Val Met Ser Tyr Ile His Ser Met Asn Ser Ser Ile Leu  
123 385 390 395 400  
124 Glu Asp Trp Asn Phe Gly Val Pro Pro Pro Thr Thr Ser Leu Val  
125 405 410 415  
126 Asp Thr Tyr Arg Phe Val Gln Ser Val Ala Ile Thr Cys Gln Lys Asp  
127 420 425 430  
128 Ala Ala Pro Ala Glu Asn Lys Asp Pro Tyr Asp Lys Leu Lys Phe Trp  
129 435 440 445  
130 Asn Val Asp Leu Lys Glu Lys Phe Ser Leu Asp Leu Asp Gln Tyr Pro  
131 450 455 460  
132 Leu Gly Arg Lys Phe Leu Val Gln Ala Gly Leu Arg Arg Lys Pro Thr  
133 465 470 475 480  
134 Ile Gly Pro Arg Lys Arg Ser Ala Pro Ser Ala Thr Thr Ser Ser Lys  
135 485 490 495  
136 Pro Ala Lys Arg Val Arg Val Arg Ala Arg Lys  
137 500 505  
140 <210> SEQ ID NO: 3  
141 <211> LENGTH: 1389  
142 <212> TYPE: DNA  
143 <213> ORGANISM: Artificial Sequence  
145 <220> FEATURE:  
146 <223> OTHER INFORMATION: HPV18 L2 Consensus Sequence  
148 <400> SEQUENCE: 3  
149 atggtatccc accgtgccgc acgacgcaaa cgggcttcgg tgactgactt atataaaaaca 60  
150 tgttaaacaat ctggtacatg tccatctgat gttgttaata aggttagaggg caccacgtta 120  
151 gcagataaaa tattgcaatg gtcaagcctt ggtatatttt tgggtggact tggcatagg 180  
152 actggaaatg gtacaggggg tcgtacaggg tacattccat tgggtggcg ttccaataca 240  
153 gttgtggatg tcggcctcac acgtcctcca gtggttattg aacctgtggg ccccacagac 300  
154 ccatctattt tacatattt agaggactca agtgtgtta catcaggtgc acctaggcct 360  
155 acttttactg gcacgtctgg gtttgatata acatctgtg gtacaactac acctgcagtt 420  
156 ttggatatac caccttcgtc tacctctgtt tctatttcca caaccaattt taccaatcct 480  
157 gcattttctg atccgtccat tattgaagtt ccacaaactg gggaggtgtc aggtaatgt 540  
158 tttgttggta cccctacatc tggAACACAT gggtatgaag aaataccttt acaaacattt 600  
159 gcttcttctg gtacggggga ggaacccatt agtagtaccc cattgcctac tttgcggcgt 660  
160 gtagcaggc cccgcctta cagtagggcc taccaacaag tttctgtggc taaccctgag 720  
161 tttcttacac gtccatcctc tttaattacc tatgacaacc cggccttga gcctgtggac 780  
162 actacattaa catttgagcc tcgttagtaat gttcctgatt cagattttat ggatatttc 840

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163 cgtttacata ggcctgctt aacatccagg cgtggtaactg tgcgccttag tagatttaggt 900  
 164 ccaaaggc aa ctatgtttac ccgtagcggt acacaaatag gtgctagggt tcacttttat 960  
 165 catgatataa gtcctattgc accctccccca gaatatattg aactgcagcc tttagtatct 1020  
 166 gccacggagg acaatggctt gtttgatata tatgcagatg acatagaccc tgcaatgcct 1080  
 167 gtaccatcgc gtcctactac ctcctctgca gtttctacat attcgccac tatatcatct 1140  
 168 gcctttccct atagtaatgt aacggtccct ttaaacctcct cttggatgt gcctgtatac 1200  
 169 acgggtcctg atattacatt accaccta actctgtat ggcccattgt atcacccaca 1260  
 170 gcccctgcct ctacacagta tatttgtata catggtacac attattattt gtggccattta 1320  
 171 tattatttta ttccctaaaaa gcgtaaacgt gttccctatt ttttgcaga tggctttgt 1380  
 172 gcgccctag 1389  
 174 <210> SEQ ID NO: 4  
 175 <211> LENGTH: 461  
 176 <212> TYPE: PRT  
 177 <213> ORGANISM: Artificial Sequence  
 179 <220> FEATURE:  
 180 <223> OTHER INFORMATION: HPV18 L2 Consensus Sequence  
 182 <400> SEQUENCE: 4  
 183 Met Val Ser His Arg Ala Ala Arg Arg Lys Arg Ala Ser Val Thr Asp  
 184 1 5 10 15  
 185 Leu Tyr Lys Thr Cys Lys Gln Ser Gly Thr Cys Pro Ser Asp Val Val  
 186 20 25 30  
 187 Asn Lys Val Glu Gly Thr Thr Leu Ala Asp Lys Ile Leu Gln Trp Ser  
 188 35 40 45  
 189 Ser Leu Gly Ile Phe Leu Gly Gly Leu Gly Ile Gly Thr Gly Ser Gly  
 190 50 55 60  
 191 Thr Gly Gly Arg Thr Gly Tyr Ile Pro Leu Gly Gly Arg Ser Asn Thr  
 192 65 70 75 80  
 193 Val Val Asp Val Gly Pro Thr Arg Pro Pro Val Val Ile Glu Pro Val  
 194 85 90 95  
 195 Gly Pro Thr Asp Pro Ser Ile Val Thr Leu Ile Glu Asp Ser Ser Val  
 196 100 105 110  
 197 Val Thr Ser Gly Ala Pro Arg Pro Thr Phe Thr Gly Thr Ser Gly Phe  
 198 115 120 125  
 199 Asp Ile Thr Ser Ala Gly Thr Thr Pro Ala Val Leu Asp Ile Thr  
 200 130 135 140  
 201 Pro Ser Ser Thr Ser Val Ser Ile Ser Thr Thr Asn Phe Thr Asn Pro  
 202 145 150 155 160  
 203 Ala Phe Ser Asp Pro Ser Ile Ile Glu Val Pro Gln Thr Gly Glu Val  
 204 165 170 175  
 205 Ser Gly Asn Val Phe Val Gly Thr Pro Thr Ser Gly Thr His Gly Tyr  
 206 180 185 190  
 207 Glu Glu Ile Pro Leu Gln Thr Phe Ala Ser Ser Gly Thr Gly Glu Glu  
 208 195 200 205  
 209 Pro Ile Ser Ser Thr Pro Leu Pro Thr Val Arg Arg Val Ala Gly Pro  
 210 210 215 220  
 211 Arg Leu Tyr Ser Arg Ala Tyr Gln Gln Val Ser Val Ala Asn Pro Glu  
 212 225 230 235 240  
 213 Phe Leu Thr Arg Pro Ser Ser Leu Ile Thr Tyr Asp Asn Pro Ala Phe  
 214 245 250 255

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215 Glu Pro Val Asp Thr Thr Leu Thr Phe Glu Pro Arg Ser Asn Val Pro  
216 260 265 270  
217 Asp Ser Asp Phe Met Asp Ile Ile Arg Leu His Arg Pro Ala Leu Thr  
218 275 280 285  
219 Ser Arg Arg Gly Thr Val Arg Phe Ser Arg Leu Gly Gln Arg Ala Thr  
220 290 295 300  
221 Met Phe Thr Arg Ser Gly Thr Gln Ile Gly Ala Arg Val His Phe Tyr  
222 305 310 315 320  
223 His Asp Ile Ser Pro Ile Ala Pro Ser Pro Glu Tyr Ile Glu Leu Gln  
224 325 330 335  
225 Pro Leu Val Ser Ala Thr Glu Asp Asn Gly Leu Phe Asp Ile Tyr Ala  
226 340 345 350  
227 Asp Asp Ile Asp Pro Ala Met Pro Val Pro Ser Arg Pro Thr Thr Ser  
228 355 360 365  
229 Ser Ala Val Ser Thr Tyr Ser Pro Thr Ile Ser Ser Ala Ser Ser Tyr  
230 370 375 380  
231 Ser Asn Val Thr Val Pro Leu Thr Ser Ser Trp Asp Val Pro Val Tyr  
232 385 390 395 400  
233 Thr Gly Pro Asp Ile Thr Leu Pro Pro Thr Ser Val Trp Pro Ile Val  
234 405 410 415  
235 Ser Pro Thr Ala Pro Ala Ser Thr Gln Tyr Ile Gly Ile His Gly Thr  
236 420 425 430  
237 His Tyr Tyr Leu Trp Pro Leu Tyr Tyr Phe Ile Pro Lys Lys Arg Lys  
238 435 440 445  
239 Arg Val Pro Tyr Phe Phe Ala Asp Gly Phe Val Ala Ala  
240 450 455 460  
243 <210> SEQ ID NO: 5  
244 <211> LENGTH: 41  
245 <212> TYPE: DNA  
246 <213> ORGANISM: Artificial Sequence  
248 <220> FEATURE:  
249 <223> OTHER INFORMATION: oligonucleotide, sense primer  
251 <400> SEQUENCE: 5  
252 gaagatctca caaaacaaaa tggctttgtg gcgccctagt g 41  
254 <210> SEQ ID NO: 6  
255 <211> LENGTH: 36  
256 <212> TYPE: DNA  
257 <213> ORGANISM: Artificial Sequence  
259 <220> FEATURE:  
260 <223> OTHER INFORMATION: oligonucleotide, antisense primer  
262 <400> SEQUENCE: 6  
263 gaagatcttt acttcctggc acgtacacgc acacgc 36  
265 <210> SEQ ID NO: 7  
266 <211> LENGTH: 45  
267 <212> TYPE: DNA  
268 <213> ORGANISM: Artificial Sequence  
270 <220> FEATURE:  
271 <223> OTHER INFORMATION: oligonucleotide, sense primer  
273 <400> SEQUENCE: 7

**VERIFICATION SUMMARY**

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Input Set : A:\19424PC Seq List.txt

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4 M:271 C: Current Filing Date differs, Replaced Current Filing Date